GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 21, 2003, 17:55:24 ; Search time 20 Seconds
(without alignments)
389.877 Million cell updates/sec

Title: US-09-527-376-2
Perfect score: 981
Sequence: 1 MTAPSCAFPVQFRQPSVSGL.....SPVGMIPDIYEKEVRLMIPL 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	511	52.1	198	1	DUSE_HUMAN	O95147 homo sapien
2	500	51.0	198	1	DUSE_MOUSE	Q9jly7 mus musculu
3	252	25.7	367	1	DUS1_HUMAN	P28562 homo sapien
4	252	25.7	367	1	DUS1_MOUSE	P28563 mus musculu
5	252	25.7	367	1	DUS1_RAT	Q64623 rattus norv
6	238	24.3	394	1	DUS4_HUMAN	Q13115 homo sapien
7	236	24.1	375	1	DUS4_CHICK	Q9pw71 gallus gall
8	236	24.1	395	1	DUS4_RAT	Q62767 rattus norv
9	233	23.8	619	1	VHP1_CAEEL	Q10038 caenorhabdi
10	230	23.4	235	1	DUSF_HUMAN	Q9h1r2 homo sapien
11	221	22.5	384	1	DUS5_HUMAN	Q16690 homo sapien
12	219.5	22.4	384	1	DUS5_RAT	O54838 rattus norv
13	219.5	22.4	625	1	DUS8_HUMAN	Q13202 homo sapien
14	212.5	21.7	663	1	DUS8_MOUSE	O09112 mus musculu
15	208.5	21.3	665	1	DUSX_HUMAN	Q9by84 homo sapien
16	208	21.2	318	1	DUS2_MOUSE	Q05922 mus musculu
17	200	20.4	482	1	DUSA_HUMAN	Q9y6w6 homo sapien
18	197	20.1	314	1	DUS2_HUMAN	Q05923 homo sapien
19	194.5	19.8	198	1	DUSD_HUMAN	Q9ui16 homo sapien
20	183.5	18.7	280	1	DUS7_RAT	Q63340 rattus norv
21	183.5	18.7	320	1	DUS7_HUMAN	Q16829 homo sapien
22	183.5	18.7	320	1	DUS7_MOUSE	Q91z46 mus musculu
23	181.5	18.5	198	1	DUSD_MOUSE	Q9qyj7 mus musculu
24	180.5	18.4	384	1	DUS9_HUMAN	Q99956 homo sapien
25	174	17.7	381	1	DUS6_HUMAN	Q16828 homo sapien
26	174	17.7	381	1	DUS6_MOUSE	Q9dbb1 mus musculu
27	174	17.7	381	1	DUS6_RAT	Q64346 rattus norv
28	165.5	16.9	292	1	YO42_CAEEL	P34680 caenorhabdi
29	162.5	16.6	185	1	DUS3_HUMAN	P51452 homo sapien
30	160	16.3	209	1	YIL3_YEAST	P40479 saccharomyc
31	159.5	16.3	185	1	DUS3_MOUSE	Q9d7x3 mus musculu
32	155	15.8	489	1	MSG5_YEAST	P38590 saccharomyc
33	151	15.4	171	1	VH01_RACVI	P80994 raccoon pox
34	147	15.0	171	1	DUSP_VACCC	P20495 vaccinia vi
35	147	15.0	171	1	DUSP_VACCV	P07239 vaccinia vi
36	144	14.7	171	1	DUSP_VARV	P33064 variola vir
37	141	14.4	340	1	DUSC_HUMAN	Q9uni6 homo sapien
38	139.5	14.2	276	1	PTP3_CHLEU	Q39491 chlamydomon
39	137	14.0	807	1	YB9T_YEAST	P38148 saccharomyc
40	120.5	12.3	178	1	DUSP_MYXVL	Q85297 myxoma viru
41	117	11.9	364	1	PVH1_YEAST	Q02256 saccharomyc
42	107	10.9	166	1	DUSP_FOWPV	Q9j592 fowlpox vir
43	107	10.9	597	1	PTPX_CANAL	P43078 candida alb
44	99	10.1	160	1	PTP2_NPVOP	O10273 orgyia pseu
45	93	9.5	430	1	YNBD_ECOLI	P76093 escherichia

ALIGNMENTS

```
RESULT 1
DUSE_HUMAN
ID   DUSE_HUMAN      STANDARD;      PRT;   198 AA.
AC   O95147;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 14 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Mitogen-activated protein kinase phosphatase 6) (MAP kinase
DE   phosphatase 6) (MKP-6) (MKP-1 like protein tyrosine phosphatase)
DE   (MKP-L).
GN   DUSP14 OR MKP6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yuan Y., Suphapeetiporn K., Sun H.;
RT   "MKP-L, a novel MKP-1 like protein tyrosine phosphatase.";
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20571897; PubMed=11123293;
RA   Marti F., Krause A., Post N.H., Lyddane C., Dupont B., Sadelain M.,
RA   King P.D.;
RT   "Negative-feedback regulation of CD28 costimulation by a novel
RT   mitogen-activated protein kinase phosphatase, MKP6.";
RL   J. Immunol. 166:197-206(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Involved in the inactivation of MAP kinases.
CC       Dephosphorylates ERK, JNK and p38 MAP-kinases.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBUNIT: Intercats with CD28.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF038844; AAD02105.1; -.
DR   EMBL; AF120032; AAF28861.1; -.
DR   EMBL; BC000370; AAH00370.1; -.
DR   EMBL; BC001894; AAH01894.1; -.
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DR   EMBL; BC004448; AAH04448.1; -.
DR   HSSP; Q16828; 1MKP.
DR   Genew; HGNC:17007; DUSP14.
DR   MIM; 606618; -.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase.
FT   DOMAIN       91    156       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE    111    111       BY SIMILARITY.
SQ   SEQUENCE   198 AA;  22255 MW;  6AAFAE1B3A24F9AA CRC64;

  Query Match             52.1%;  Score 511;  DB 1;  Length 198;
  Best Local Similarity   50.3%;  Pred. No. 6.9e-44;
  Matches   90;  Conservative   40;  Mismatches   49;  Indels    0;  Gaps    0;

Qy       9 PVQFRQPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDIQYMQ 68
           |     :  : |::||| ||::   |  |:|: :| :  || ::| ::|: |  :   :|::
Db      16 PRMISEGDIGGIAQITSSLFLGRGSVASNRHLLQARGITCIVNATIEIPNFNWPQFEYVR 75

Qy      69 VPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHAMSLL 128
           ||:|| |:: :  :|| :|| |||   | | ||:|||||||||| ||:|||||:| : ||
Db      76 VPLADMPHAPIGLYFDTVADKIHSVSRKHGATLVHCAAGVSRSATLCIAYLMKFHNVCLL 135

Qy     129 DAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPVGMIPDIYEKEVRLMIP 187
           :|: | |: ||:|||| ||| ||| || |||||:|| || :| |::||:|||| | ::|
Db     136 EAYNWVKARRPVIRPNVGFWRQLIDYERQLFGKSTVKMVQTPYGIVPDVYEKESRHLMP 194


RESULT 2
DUSE_MOUSE
ID   DUSE_MOUSE     STANDARD;      PRT;   198 AA.
AC   Q9JLY7; Q9D715;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 14 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Mitogen-activated protein kinase phosphatase 6) (MAP kinase
DE   phosphatase 6) (MKP-6).
GN   DUSP14 OR MKP6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=20571897; PubMed=11123293;
RA   Marti F., Krause A., Post N.H., Lyddane C., Dupont B., Sadelain M.,
RA   King P.D.;
RT   "Negative-feedback regulation of CD28 costimulation by a novel
RT   mitogen-activated protein kinase phosphatase, MKP6.";
RL   J. Immunol. 166:197-206(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Involved in the inactivation of MAP kinases.
CC       Dephosphorylates ERK, JNK and p38 MAP-kinases.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF120113; AAF28862.1; -.
DR   EMBL; AK009744; BAB26474.1; -.
DR   EMBL; BC002130; AAH02130.1; -.
DR   HSSP; Q16828; 1MKP.
DR   MGD; MGI:1927168; Dusp14.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase.
FT   DOMAIN       91    156       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE    111    111       BY SIMILARITY.
FT   CONFLICT     38     38       R -> K (IN REF. 1).
FT   CONFLICT    150    150       P -> H (IN REF. 1).
FT   CONFLICT    160    160       D -> E (IN REF. 1).
FT   CONFLICT    163    163       S -> R (IN REF. 1).
SQ   SEQUENCE   198 AA;  22311 MW;  5C2B4210E886DFCF CRC64;

  Query Match             51.0%;  Score 500;  DB 1;  Length 198;
  Best Local Similarity   50.8%;  Pred. No. 8.7e-43;
  Matches   91;  Conservative   37;  Mismatches   51;  Indels    0;  Gaps    0;

Qy       9 PVQFRQPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDIQYMQ 68
           |     :  : |::||| ||::    |:|  :| :  || ||| ::|: |  :   :|::
Db      16 PRMISEGDIGGIAQITSSLFLGRASVASNWHLLQARGITCVINATIEIPNFNWPQFEYVK 75

Qy      69 VPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHAMSLL 128
           ||:|| |:: :  :|| :|| ||||  | | ||:|||||||||| ||:|||||:| : ||
Db      76 VPLADIPHAPIRLYFDTVADKIHSVSKKHGATLVHCAAGVSRSATLCIAYLMKFHNLCLL 135

Qy     129 DAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPVGMIPDIYEKEVRLMIP 187
           :|: | |: ||:|||| ||| ||| || |||||::| || :| |::|||:|||| | ::|
Db     136 EAYNWVKARRPVIRPNLGFWRQLIDYESQLFGKSSVKMVQTPYGIIPDVYEKESRHLMP 194


RESULT 3
DUS1_HUMAN
ID   DUS1_HUMAN     STANDARD;      PRT;   367 AA.
AC   P28562;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
```

```
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 1 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (MAP kinase phosphatase-1) (MKP-1) (Protein-tyrosine phosphatase
DE   CL100) (Dual specificity protein phosphatase hVH1).
GN   DUSP1 OR PTPN10 OR MKP1 OR CL100 OR VH1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Foreskin;
RX   MEDLINE=93024952; PubMed=1406996;
RA   Keyes S.M., Emslie E.A.;
RT   "Oxidative stress and heat shock induce a human gene encoding a
RT   protein-tyrosine phosphatase.";
RL   Nature 359:644-647(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP
CC       KINASE ERK2 ON BOTH THR-183 AND TYR-185.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- INDUCTION: BY OXIDATIVE STRESS AND HEAT SHOCK.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X68277; CAA48338.1; -.
DR   EMBL; BC022463; AAH22463.1; -.
DR   PIR; S29090; S29090.
DR   HSSP; Q16828; 1MKP.
DR   Genew; HGNC:3064; DUSP1.
DR   MIM; 600714; -.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00581; Rhodanese; 1.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Cell cycle.
FT   DOMAIN        9    135       RHODANESE.
FT   DOMAIN      175    367       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE    258    258       BY SIMILARITY.
SQ   SEQUENCE   367 AA;  39297 MW;  11BD1D39A9FCD51F CRC64;

  Query Match             25.7%;  Score 252;  DB 1;  Length 367;
  Best Local Similarity   34.3%;  Pred. No. 1.1e-17;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels    4;  Gaps    1;

Qy       5 SCAPPVQFRQPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDI 64
           ||: |:        |  :|   ||: :   |: | || :  || :||||    |
Db     163 SCSTPLY----DQGGPVEILPFLYLGSAYHASRKDMLDALGITALINVSANCPNHFEGHY 218

Qy      65 QYMQVPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHA 124
             ||  :|| |:  : :  :|:   | | |::   ||  :|| ||:|||| :||||||: :
Db     219 QYKSIPVEDNHKADISSWFNEAIDFIDSIKNAGGRVFVHCQAGISRSATICLAYLMRTNR 278

Qy     125 MSLLDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPVGMIPD 176
           : | :|  : |  | || ||  |  ||: :| |:   :      ||   : |
Db     279 VKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPHCSAEAGSPAMAVLD 330


RESULT 4
DUS1_MOUSE
ID   DUS1_MOUSE     STANDARD;      PRT;   367 AA.
AC   P28563;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 1 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (MAP kinase phosphatase-1) (MKP-1) (Protein-tyrosine phosphatase
DE   3CH134) (Protein-tyrosine phosphatase ERP).
GN   DUSP1 OR PTPN10 OR MKP1 OR 3CH134 OR PTPN16.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=92158357; PubMed=1741163;
RA   Charles C.H., Abler A.S., Lau L.F.;
RT   "cDNA sequence of a growth factor-inducible immediate early gene and
RT   characterization of its encoded protein.";
RL   Oncogene 7:187-190(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93360956; PubMed=8355678;
RA   Noguchi T., Metz R., Chen L., Mattei M.-G., Carrasco D., Bravo R.;
RT   "Structure, mapping, and expression of erp, a growth factor-inducible
RT   gene encoding a nontransmembrane protein tyrosine phosphatase, and
RT   effect of ERP on cell growth.";
RL   Mol. Cell. Biol. 13:5195-5205(1993).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=94037096; PubMed=8221888;
RA   Sun H., Charles C.H., Lau L.F., Tonks N.K.;
RT   "MKP-1 (3CH134), an immediate early gene product, is a dual
RT   specificity phosphatase that dephosphorylates MAP kinase in vivo.";
RL   Cell 75:487-493(1993).
CC   -!- FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP
CC       KINASE ERK2 ON BOTH THR-183 AND TYR-185.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- INDUCTION: BY GROWTH FACTORS.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X61940; CAA43944.1; -.
DR   EMBL; S64851; AAB27882.1; -.
DR   PIR; S24411; S24411.
DR   HSSP; Q16828; 1MKP.
DR   MGD; MGI:105120; Ptpn16.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
```

```
DR   Pfam; PF00581; Rhodanese; 1.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Cell cycle.
FT   DOMAIN        9    135       RHODANESE.
FT   DOMAIN      175    367       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE    258    258
FT   MUTAGEN     258    258       C->S: LOSS OF ACTIVITY.
SQ   SEQUENCE   367 AA;  39369 MW;  50B5F90FEBBD19AB CRC64;

  Query Match             25.7%;  Score 252;  DB 1;  Length 367;
  Best Local Similarity   34.3%;  Pred. No. 1.1e-17;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels    4;  Gaps    1;

Qy       5 SCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDI 64
           ||: |:        |  :|   ||: :   |: | || :  || :|||   |
Db     163 SCSTPLY----DQGGPVEILSFLYLGSAYHASRKDMLDALGITALINVSANCPNHFEGHY 218

Qy      65 QYMQVPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHA 124
             ||  :|| |:  : :  :|:   | | |::   ||  :|| ||:|||| :||||||: :
Db     219 QYKSIPVEDNHKADISSWFNEAIDFIDSIKDAGGRVFVHCQAGISRSATICLAYLMRTNR 278

Qy     125 MSLLDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPVGMIPD 176
           : | :|  : |  | || ||  |  ||: :| |:   :      ||   : |
Db     279 VKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPHCSAEAGSPAMAVLD 330


RESULT 5
DUS1_RAT
ID   DUS1_RAT       STANDARD;      PRT;   367 AA.
AC   Q64623;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 1 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (MAP kinase phosphatase-1) (MKP-1) (Protein-tyrosine phosphatase
DE   CL100).
GN   DUSP1 OR CL100.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Lung;
RA   Muda M., Schlegel W., Arkinstall S.;
RL   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP
CC       KINASE ERK2 ON BOTH THR-183 AND TYR-185.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X84004; CAA58828.1; -.
DR   HSSP; Q16828; 1MKP.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00581; Rhodanese; 1.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Cell cycle.
FT   DOMAIN        9    135       RHODANESE.
FT   DOMAIN      175    367       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE    258    258       BY SIMILARITY.
SQ   SEQUENCE   367 AA;  39541 MW;  5112ADF290499139 CRC64;

  Query Match             25.7%;  Score 252;  DB 1;  Length 367;
  Best Local Similarity   34.3%;  Pred. No. 1.1e-17;
  Matches   59;  Conservative   29;  Mismatches   80;  Indels    4;  Gaps    1;

Qy       5 SCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDI 64
           ||: |:        |  :|   ||: :   |: | || :  || :|||   |
Db     163 SCSTPLY----DQGGPVEILSFLYLGSAYHASRKDMLDALGITALINVSANCPNHFEGHY 218

Qy      65 QYMQVPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHA 124
             ||  :|| |:  : :  :|:   | | |::   ||  :|| ||:|||| :||||||: :
Db     219 QYKSIPVEDNHKADISSWFNEAIDFIDSIKDAGGRVFVHCQAGISRSATICLAYLMRTNR 278

Qy     125 MSLLDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPVGMIPD 176
           : | :|  : |  | || ||  |  ||: :| |:   :      ||   : |
Db     279 VKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPHCSAEAGSPAMAVLD 330


RESULT 6
DUS4_HUMAN
ID   DUS4_HUMAN     STANDARD;      PRT;   394 AA.
AC   Q13115; Q13524;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Mitogen-activated protein kinase phosphatase-2) (MAP kinase
DE   phosphatase-2) (MKP-2) (Dual specificity protein phosphatase hVH2).
GN   DUSP4 OR MKP2 OR VH2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95221370; PubMed=7535768;
RA   Guan K.-L., Butch E.;
RT   "Isolation and characterization of a novel dual specific phosphatase,
RT   HVH2, which selectively dephosphorylates the mitogen-activated
RT   protein kinase.";
RL   J. Biol. Chem. 270:7197-7203(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96198119; PubMed=8626452;
RA   Chu Y., Solski P.A., Khosravi-Far R., Der C.J., Kelly K.;
RT   "The mitogen-activated protein kinase phosphatases PAC1, MKP-1, and
RT   MKP-2 have unique substrate specificities and reduced activity in vivo
RT   toward the ERK2 sevenmaker mutation.";
RL   J. Biol. Chem. 271:6497-6501(1996).
CC   -!- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
CC       DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
CC       ERK1 AND ERK2.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
```

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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U21108; AAA85119.1; -.
DR   EMBL; U48807; AAC50452.1; -.
DR   HSSP; Q16828; 1MKP.
DR   Genew; HGNC:3070; DUSP4.
DR   MIM; 602747; -.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00581; Rhodanese; 1.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Nuclear protein.
FT   DOMAIN       33    157       RHODANESE.
FT   DOMAIN      197    394       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE    280    280       BY SIMILARITY.
FT   CONFLICT    111    111       R -> G (IN REF. 2).
SQ   SEQUENCE   394 AA;  42953 MW;  0603971759B6952E CRC64;

  Query Match             24.3%;  Score 238;  DB 1;  Length 394;
  Best Local Similarity   33.9%;  Pred. No. 2.9e-16;
  Matches   57;  Conservative   30;  Mismatches   77;  Indels    4;  Gaps    1;

Qy       5 SCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDI 64
           ||  |:      |  :|    ||: :   |  : || :  || ::||| :  |
Db     185 SCGTPLH----DQGGPVEILPFLYLGSAYHAARRDMLDALGITALLNVSSDCPNHFEGHY 240

Qy      65 QYMQVPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHA 124
           ||  :|| |:  : :  :|    ::| :|:  :|| |:|| ||:|||| :|||||
Db     241 QYKCIPVEDNHKADISSWFMEAIEYIDAVKDCRGRVLVHCQAGISRSATICLAYLMMKKR 300

Qy     125 MSLLDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPVG 172
           : | :|  : |  | || ||  |  ||: :| |:   :     :|| |
Db     301 VRLEEAFEFVKQRRSIISPNFSFMGQLLQFESQVLATSCAAEAASPSG 348


RESULT 7
DUS4_CHICK
ID   DUS4_CHICK     STANDARD;      PRT;   375 AA.
AC   Q9PW71;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Mitogen-activated protein kinase phosphatase-2) (MAP kinase
DE   phosphatase-2) (MKP-2).
GN   DUSP4 OR MKP2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=White leghorn;
RX   MEDLINE=20379359; PubMed=10918612;
RA   Fu S.-L., Waha A., Vogt P.K.;
RT   "Identification and characterization of genes upregulated in cells
RT   transformed by v-Jun.";
RL   Oncogene 19:3537-3545(2000).
CC   -!- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
CC       DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
CC       ERK1 AND ERK2 (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF167296; AAD46656.1; -.
DR   HSSP; Q16828; 1MKP.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00581; Rhodanese; 1.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Nuclear protein.
FT   DOMAIN       15    141       RHODANESE.
FT   DOMAIN      178    375       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE    261    261       BY SIMILARITY.
SQ   SEQUENCE   375 AA;  41052 MW;  179290D0C2BEEEF1 CRC64;

  Query Match             24.1%;  Score 236;  DB 1;  Length 375;
  Best Local Similarity   34.1%;  Pred. No. 4.3e-16;
  Matches   58;  Conservative   28;  Mismatches   80;  Indels    4;  Gaps    1;

Qy       5 SCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDI 64
           ||  |:      |  :|    ||: :   |  : || :  || ::||| :  |
Db     166 SCGTPLH----DQGGPVEILPFLYLGSAYHAARRDMLDALGITALLNVSSDCPNHFEGHY 221

Qy      65 QYMQVPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHA 124
           ||  :|| |:  : :  :|    ::| ||:   || |:|| ||:|||| :||||||
Db     222 QYKCIPVEDNHKADISSWFMEAIEYIDSVKECCGRVLVHCQAGISRSATICLAYLMMKKR 281

Qy     125 MSLLDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPVGMI 174
           : |  |  : |  | || ||  |  ||: :| |:   :     :|| | :
Db     282 VKLEKAFEFVKQRRSIISPNFSFMGQLLQFESQVLATSCAVEAASPSGTL 331


RESULT 8
DUS4_RAT
ID   DUS4_RAT       STANDARD;      PRT;   395 AA.
AC   Q62767;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Mitogen-activated protein kinase phosphatase-2) (MAP kinase
DE   phosphatase-2) (MKP-2).
GN   DUSP4 OR MKP2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pheochromocytoma;
RX   MEDLINE=95301550; PubMed=7782322;
```

```
RA   Misra-Press A., Rim C.S., Yao H., Roberson M.S., Stork P.J.S.;
RT   "A novel mitogen-activated protein kinase phosphatase. Structure,
RT   expression, and regulation.";
RL   J. Biol. Chem. 270:14587-14596(1995).
CC   -!- FUNCTION: REGULATES MITOGENIC SIGNAL TRANSDUCTION BY
CC       DEPHOSPHORYLATING BOTH THR AND TYR RESIDUES ON MAP KINASES
CC       ERK1 AND ERK2 (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- TISSUE SPECIFICITY: EXPRESSED AT MODERATE LEVELS IN NEARLY ALL
CC       TISSUES AND CELLS INCLUDING BRAIN, SPLEEN, AND TESTES WITH THE
CC       HIGHER EXPRESSION IN THE HEART AND LUNG AND LOWER EXPRESSION IN
CC       SKELETAL MUSCLE AND KIDNEY. UNDETECTABLE IN LIVER. EXPRESSED IN
CC       MANY AREAS OF THE BRAIN WITH VERY STRONG EXPRESSION IN THE
CC       HIPPOCAMPUS, PIRIFORM CORTEX, AND THE SUPRACHIASMATIC NUCLEUS.
CC   -!- INDUCTION: BY MITOGENS AND BY STRESS.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U23438; AAC52493.1; -.
DR   HSSP; Q16828; 1MKP.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00581; Rhodanese; 1.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Nuclear protein.
FT   DOMAIN       34    158       RHODANESE.
FT   DOMAIN      198    395       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE    281    281       BY SIMILARITY.
SQ   SEQUENCE   395 AA;  43187 MW;  A90EFFD378A050FD CRC64;

  Query Match             24.1%;  Score 236;  DB 1;  Length 395;
  Best Local Similarity   33.9%;  Pred. No. 4.6e-16;
  Matches   57;  Conservative   30;  Mismatches   77;  Indels    4;  Gaps    1;

Qy       5 SCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDI 64
           ||  |:         |  :|   ||: :   |  : || :  || ::||| :  |
Db     186 SCGTPLH----DQGGPVEILPFLYLGSAYHAARRDMLDALGITALLNVSSDCPNHFEGHY 241

Qy      65 QYMQVPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHA 124
           ||  :|| |:  : :  :|    ::| :|:  :|| |:|| ||:|||| :||||||
Db     242 QYKCIPVEDNHKADISSWFMEAIEYIDAVKDCRGRVLVHCQAGISRSATICLAYLMMKKR 301

Qy     125 MSLLDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPVG 172
           : | :|  : |  | || ||  |  ||: :| |:   :     :|| |
Db     302 VRLEEAFEFVKQRRSIISPNFSFMGQLLQFESQVLTTSCAAEAASPSG 349


RESULT 9
VHP1_CAEEL
ID   VHP1_CAEEL     STANDARD;      PRT;   619 AA.
AC   Q10038;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein-tyrosine phosphatase vhp-1 (EC 3.1.3.48).
GN   VHP-1 OR F08B1.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Chissoe S.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U23178; AAC46719.1; -.
DR   HSSP; Q16828; 1MKP.
DR   WormPep; F08B1.1; CE01899.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase.
FT   DOMAIN      200    269       PROTEIN-TYROSINE PHOSPHATASE.
FT   DOMAIN       92     95       POLY-SER.
FT   DOMAIN      351    354       POLY-SER.
FT   DOMAIN      465    472       POLY-SER.
FT   DOMAIN      483    488       POLY-SER.
FT   ACT_SITE    224    224       BY SIMILARITY.
SQ   SEQUENCE   619 AA;  66354 MW;  369E326F615D0529 CRC64;

  Query Match             23.8%;  Score 233;  DB 1;  Length 619;
  Best Local Similarity   33.3%;  Pred. No. 1.6e-15;
  Matches   48;  Conservative   35;  Mismatches   59;  Indels    2;  Gaps    1;

Qy      14 QPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNT--LYEDIQYMQVPV 71
           ||:  |:: || ::|: : : : :: || :  |::|||:|:    :  : ||  :|::||
Db     132 QPTGDGITLITPNIYLGSQIDSLDETMLDALDISVVINLSMTCPKSVCIKEDKNFMRIPV 191

Qy      72 ADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHAMSLLDAH 131
           ||   :|  :|    : :         : |:|| ||:|||  | ::|:|:|  |   ||:
Db     192 NDSYQEKLSPYFPMAYEFLEKCRRAGKKCLIHCLAGISRSPTLAISYIMRYMKMGSDDAY 251

Qy     132 TWTKSCRPIIRPNSGFWEQLIHYE 155
           : |  || | ||  |  ||: ||
Db     252 RYVKERRPSISPNFNFMGQLLEYE 275


RESULT 10
DUSF_HUMAN
ID   DUSF_HUMAN     STANDARD;      PRT;   235 AA.
AC   Q9H1R2;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 15 (EC 3.1.3.48) (EC 3.1.3.16).
GN   DUSP15.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052;
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL160175; CAC10008.2; ALT_SEQ.
DR   HSSP; P51452; 1VHR.
DR   Genew; HGNC:16236; DUSP15.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00782; DSPc; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase.
FT   DOMAIN       65    133       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE     88     88       BY SIMILARITY.
SQ   SEQUENCE   235 AA;  26152 MW;  A3AF26789894FECB CRC64;

  Query Match           23.4%;  Score 230;  DB 1;  Length 235;
  Best Local Similarity  31.4%;  Pred. No. 9.5e-16;
  Matches   55;  Conservative   34;  Mismatches   76;  Indels   10;  Gaps    3;

Qy      18 SGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNS 77
           :|:::   ||: | : | :   |  |:|| :|::  |    | :|| |:::|||||:|
Db       3 NGMTKVLPGLYLGNFIDAKDLDQLGRNKITHIISIH-ESPQPLLQDITYLRIPVADTPEV 61

Qy      78 RLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHAMSLLDAHTWTKSC 137
            :   |    : ||   :  |  |:|| ||:|||  :  ||:|   :    |     |:
Db      62 PIKKHFKECINFIHCCRLNGGNCLVHCFAGISRSTTIVTAYVMTVTGLGWRDVLEAIKAT 121

Qy     138 RPIIRPNSGFWEQLIHYEFQLFG----KNTVHMVSSPVGMIPDIYEKEVRLMIPL 188
           |||  || || :||     : ||    :     :    |  |   |:|:| ::||
Db     122 RPIANPNPGFRQQL-----EEFGWASSQKLRRQLEERFGESPFRDEEELRALLPL 171


RESULT 11
DUS5_HUMAN
ID   DUS5_HUMAN     STANDARD;      PRT;   384 AA.
AC   Q16690; Q12997;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 5 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Dual specificity protein phosphatase hVH3).
GN   DUSP5 OR VH3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=95138103; PubMed=7836374;
RA   Kwak S.P., Dixon J.E.;
RT   "Multiple dual specificity protein tyrosine phosphatases are
RT   expressed and regulated differentially in liver cell lines.";
RL   J. Biol. Chem. 270:1156-1160(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Mammary gland;
RX   MEDLINE=95050849; PubMed=7961985;
RA   Ishibashi T., Bottaro D.P., Michieli P., Kelley C.A.,
RA   Aaronson S.A.;
RT   "A novel dual specificity phosphatase induced by serum stimulation
RT   and heat shock.";
RL   J. Biol. Chem. 269:29897-29902(1994).
RN   [3]
RP   REVISIONS.
RA   Bottaro D.P.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: DISPLAYS PHOSPHATASE ACTIVITY TOWARD SEVERAL SUBSTRATES.
CC       THE HIGHEST RELATIVE ACTIVITY IS TOWARD ERK1.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U16996; AAB06261.1; -.
DR   EMBL; U15932; AAA64693.2; -.
DR   HSSP; Q16828; 1MKP.
DR   Genew; HGNC:3071; DUSP5.
DR   MIM; 603069; -.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00581; Rhodanese; 1.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Nuclear protein.
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FT   DOMAIN        7    139       RHODANESE.
FT   DOMAIN      180    384       PROTEIN-TYROSINE PHOSPHATASE.
FT   DOMAIN       53     74       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN       79     82       POLY-GLY.
FT   ACT_SITE    263    263       BY SIMILARITY.
FT   CONFLICT      9     11       RQL -> GHV (IN REF. 2).
FT   CONFLICT     71     71       A -> R (IN REF. 2).
FT   CONFLICT    105    106       AR -> F (IN REF. 2).
SQ   SEQUENCE   384 AA;  42107 MW;  D2B726F7C0414306 CRC64;

  Query Match             22.5%;  Score 221;  DB 1;  Length 384;
  Best Local Similarity   34.3%;  Pred. No. 1.4e-14;
  Matches   48;  Conservative   24;  Mismatches   68;  Indels    0;  Gaps    0;

Qy      19 GLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSR 78
           |  :|   ||: :   |:    |::  || ::|||          : |  :|| ||  :
Db     178 GPVEILPFLYLGSAYHASKCEFLANLHITALLNVSRRTSEACMTHLHYKWIPVEDSHTAD 237

Qy      79 LCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHAMSLLDAHTWTKSCR 138
           :   |    | |  |  | |: |:|| ||:|||  :|:|||||     | :|  : |  |
Db     238 ISSHFQEAIDFIDCVREKGGKVLVHCEAGISRSPTICMAYLMKTKQFRLKEAFDYIKQRR 297

Qy     139 PIIRPNSGFWEQLIHYEFQL 158
           :: || ||  ||: || ::
Db     298 SMVSPNFGFMGQLLQYESEI 317


RESULT 12
DUS5_RAT
ID   DUS5_RAT       STANDARD;      PRT;   384 AA.
AC   O54838;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 5 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (MAP-kinase phosphatase CPG21).
GN   DUSP5.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RX   MEDLINE=98364306; PubMed=9699150;
RA   Hevroni D., Rattner A., Bundman M., Lederfein D., Gabarah A.,
RA   Mangelus M., Silverman M.A., Kedar H., Naor C., Kornuc M., Hanoch T.,
RA   Seger R., Theill L.E., Nedivi E., Richter-Levin G., Citri Y.;
RT   "Hippocampal plasticity involves extensive gene induction and multiple
RT   cellular mechanisms.";
RL   J. Mol. Neurosci. 10:75-98(1998).
CC   -!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
CC       PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
CC       SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF013144; AAB94858.1; -.
DR   HSSP; Q16828; 1MKP.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00581; Rhodanese; 1.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Nuclear protein.
FT   DOMAIN        7    139       RHODANESE.
FT   DOMAIN      180    384       PROTEIN-TYROSINE PHOSPHATASE.
FT   DOMAIN       53     74       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT   DOMAIN       79     82       POLY-GLY.
FT   ACT_SITE    263    263       BY SIMILARITY.
SQ   SEQUENCE   384 AA;  42094 MW;  5644069B8D348700 CRC64;

  Query Match             22.4%;  Score 219.5;  DB 1;  Length 384;
  Best Local Similarity   32.5%;  Pred. No. 2e-14;
  Matches   51;  Conservative   26;  Mismatches   73;  Indels    7;  Gaps    1;

Qy      19 GLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSR 78
           |  :|   ||: :   |:    |::  || ::|||          : |  :|| ||  :
Db     178 GPVEILPFLYLGSAYHASKCEFLANLHITALLNVSRRTSEACTTHLHYKWIPVEDSHTAD 237

Qy      79 LCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALCLAYLMKYHAMSLLDAHTWTKSCR 138
           :   |    | |  |  : |: |:|| ||||||  :|:|||||     | :|  : |  |
Db     238 ISSHFQEAIDFIDCVREEGGKVLVHCEAGVSRSPTICMAYLMKTKQFRLKEAFEYIKQRR 297

Qy     139 PIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPVGMIP 175
           :: || ||  ||: || ::      : |:|    |
Db     298 SVVSPNFGFMGQLLQYESEI-------LPSTPTPQPP 327


RESULT 13
DUS8_HUMAN
ID   DUS8_HUMAN     STANDARD;      PRT;   625 AA.
AC   Q13202;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Dual specificity protein phosphatase hVH-5).
GN   DUSP8 OR VH5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RX   MEDLINE=96009533; PubMed=7561881;
RA   Martell K.J., Seasholtz A.F., Kwak S.P., Clemens K.K., Dixon J.E.;
RT   "hVH-5: a protein tyrosine phosphatase abundant in brain that
RT   inactivates mitogen-activated protein kinase.";
RL   J. Neurochem. 65:1823-1833(1995).
CC   -!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
CC       PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
CC       SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- TISSUE SPECIFICITY: ABUNDANT IN BRAIN, HEART, AND SKELETAL MUSCLE.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U27193; AAA83151.1; -.
DR   HSSP; Q16828; 1MKP.
DR   Genew; HGNC:3074; DUSP8.
DR   MIM; 602038; -.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Nuclear protein.
FT   DOMAIN       13    136       RHODANESE.
FT   DOMAIN      162    430       PROTEIN-TYROSINE PHOSPHATASE.
FT   DOMAIN      310    550       PRO-RICH.
FT   ACT_SITE    246    246       BY SIMILARITY.
SQ   SEQUENCE   625 AA;  65840 MW;  DCBEA14487219666 CRC64;

  Query Match             22.4%;  Score 219.5;  DB 1;  Length 625;
  Best Local Similarity   31.7%;  Pred. No. 3.7e-14;
  Matches   51;  Conservative   35;  Mismatches   62;  Indels   13;  Gaps    3;

Qy       4 PSCAFPVQFRQPSVS----GLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNT 59
           |:   |:   || :     ||::|   ||: :     || ::: | |: |:| |    |:
Db     141 PAALLPMSLSQPCLPVPSVGLTRILPHLYLGSQKDVLNKDLMTQNGISYVLNAS----NS 196

Qy      60 LYE-----DIQYMQVPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAAL 114
             :     : ::|:||: |:   :|  : |   : |   ::   : ::|| ||:|||| :
Db     197 CPKPDFICESRFMRVPINDNYCEKLLPWLDKSIEFIDKAKLSSCQVIVHCLAGISRSATI 256

Qy     115 CLAYLMKYHAMSLLDAHTWTKSCRPIIRPNSGFWEQLIHYE 155
           :||:||   ||  ||: : |  || | ||  |  ||: ||
Db     257 AIAYIMKTMGMSSDDAYRFVKDRRPSISPNFNFLGQLLEYE 297


RESULT 14
DUS8_MOUSE
ID   DUS8_MOUSE     STANDARD;      PRT;   663 AA.
AC   O09112;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Neuronal tyrosine threonine phosphatase 1).
GN   DUSP8 OR NTTP1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96311565; PubMed=8733137;
RA   Theodosiou A.M., Rodrigues N.R., Nesbit M.A., Ambrose H.J.,
RA   Paterson H., McLellan-Arnold E., Boyd Y., Leversha M.A., Owen N.,
RA   Blake D.J., Ashworth A., Davies K.E.;
RT   "A member of the MAP kinase phosphatase gene family in mouse
RT   containing a complex trinucleotide repeat in the coding region.";
RL   Hum. Mol. Genet. 5:675-684(1996).
CC   -!- FUNCTION: THIS PROTEIN SHOWS BOTH ACTIVITY TOWARD TYROSINE-PROTEIN
CC       PHOSPHATE AS WELL AS WITH SERINE/THREONINE-PROTEIN PHOSPHATE (BY
CC       SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN AND LUNG.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X95518; CAA64772.1; -.
DR   HSSP; Q16828; 1MKP.
DR   MGD; MGI:106626; Nttp1.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00782; DSPc; 1.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Nuclear protein.
FT   DOMAIN       13    136       RHODANESE.
FT   DOMAIN      162    432       PROTEIN-TYROSINE PHOSPHATASE.
FT   DOMAIN      452    459       POLY-ARG.
FT   DOMAIN      555    558       POLY-SER.
FT   DOMAIN      559    576       POLY-GLY.
FT   DOMAIN      577    600       POLY-SER.
FT   DOMAIN      311    552       PRO-RICH.
FT   ACT_SITE    246    246       BY SIMILARITY.
SQ   SEQUENCE   663 AA;  68847 MW;  416F429A12C1FA7C CRC64;

  Query Match             21.7%;  Score 212.5;  DB 1;  Length 663;
  Best Local Similarity   32.9%;  Pred. No. 2e-13;
  Matches   55;  Conservative   34;  Mismatches   59;  Indels   19;  Gaps    5;

Qy       2 TAPSCA-----FPVQFRQPSVSGLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEV 56
             | || :       ||    ||| ||::|   ||: :     || ::: | |: |:| |
Db     143 TLPSMSLSQPCLPV----PSV-GLTRILPHLYLGSQKDVLNKDLMTQNGISYVLNAS--- 194

Qy      57 VNTLYE-----DIQYMQVPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRS 111
            |:  :     : ::|::|: |:   :|  : |   : |   ::   : ::|| ||:|||
Db     195 -NSCPKPDFICESRFMRIPINDNYCEKLLPWLDKSIEFIDKAKLSSCQVIVHCLAGISRS 253

Qy     112 AALCLAYLMKYHAMSLLDAHTWTKSCRPIIRPNSGFWEQLIHYEFQL 158
           | : :||:||   ||  ||: : |  || | ||  |  ||: ||  |
Db     254 ATIAIAYIMKTMGMSSDDAYRFVKDRRPSISPNFNFLGQLLEYERSL 300


RESULT 15
DUSX_HUMAN
ID   DUSX_HUMAN     STANDARD;      PRT;   665 AA.
AC   Q9BY84; Q9C0G3;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Dual specificity protein phosphatase 17 (EC 3.1.3.48) (EC 3.1.3.16)
DE   (Mitogen-activated protein kinase phosphatase 7) (MAP kinase
DE   phosphatase 7) (MKP-7).
GN   MKP7 OR KIAA1700.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21486429; PubMed=11489891;
RA   Masuda K., Shima H., Watanabe M., Kikuchi K.;
RT   "MKP-7, a novel mitogen-activated protein kinase phosphatase,
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RT   functions as a shuttle protein.";
RL   J. Biol. Chem. 276:39002-39011(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21082932; PubMed=11214970;
RA   Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XIX.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:347-355(2000).
CC   -!- FUNCTION: Involved in the inactivation of MAP kinases.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB052156; BAB40814.1; -.
DR   EMBL; AB051487; BAB21791.1; ALT_INIT.
DR   HSSP; Q16828; 1MKP.
DR   InterPro; IPR000340; DS_phosphatase.
DR   InterPro; IPR001763; Rhodanese-like.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   Pfam; PF00581; Rhodanese; 2.
DR   Pfam; PF00782; DSPc; 2.
DR   SMART; SM00195; DSPc; 1.
DR   SMART; SM00012; PTPc_DSPc; 1.
DR   SMART; SM00450; RHOD; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR   PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
KW   Hydrolase; Nuclear protein.
FT   DOMAIN       11    131       RHODANESE.
FT   DOMAIN      227    289       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE    244    244       BY SIMILARITY.
SQ   SEQUENCE   665 AA;  73101 MW;  1BD853FF08460DFF CRC64;

  Query Match             21.3%;  Score 208.5;  DB 1;  Length 665;
  Best Local Similarity   33.8%;  Pred. No. 5e-13;
  Matches   54;  Conservative   25;  Mismatches   68;  Indels   13;  Gaps    3;

Qy       5 SCAFPVQFRQPSVS----GLSQITKSLYISNGVAANNKLMLSSNQITMVINVSVEVVNT- 59
           |   |    || :     | ::|  :||:       || ::  | |  |:| |    ||
Db     140 STLVPTCISQPCLPVANIGPTRILPNLYLGCQRDVLNKELMQQNGIGYVLNAS----NTC 195

Qy      60 ----LYEDIQYMQVPVADSPNSRLCDFFDPIADHIHSVEMKQGRTLLHCAAGVSRSAALC 115
                :  :::||| ||   ::  : |   | |   :   |  |:|| ||:|||| :
Db     196 PKPDFIPESHFLRVPVNDSFCEKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRSATIA 255

Qy     116 LAYLMKYHAMSLLDAHTWTKSCRPIIRPNSGFWEQLIHYE 155
           :||:||   ||| :|: : |  || | ||  |  ||: ||
Db     256 IAYIMKRMDMSLDEAYRFVKEKRPTISPNFNFLGQLLDYE 295


Search completed: April 21, 2003, 18:33:12
Job time : 22 secs
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